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Reviewer: Anne Corrigan

Timestamp: Wed Jun 13 09:40:20 EDT 2007

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Application No: 10586045

Version No: 1.1

Input Set:

Output Set:

Started: 2007-06-13 09:40:02.726

Finished: 2007-06-13 09:40:03.821

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 95 ms

Total Warnings: 31

Total Errors: 0

No. of SeqIDs Defined: 45

Actual SeqID Count: 45

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W 213	Artificial or Unknown found in <213> in SEQ ID (15)
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Input Set:

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Started: 2007-06-13 09:40:02.726
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Total Errors: 0
No. of SeqIDs Defined: 45
Actual SeqID Count: 45

Error code

Error Description

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SEQUENCE LISTING

<110> Korea Research Institute of Bioscience and Biotechnology
 Sohn, Jung-Hoon
 Choi, Eui-Sung
 Bae, Jung-Hoon
 Lee, Eung-Suck
 Shin, Mi-Kyung

<120> Rapid screening method of translational fusion partners for
 producing recombinant proteins and translational fusion partners
 screened therefrom

<130> 2472.0010000

<140> US 10/586,045

<141> 2006-07-14

<150> PCT/KR2004/003517

<151> 2004-12-30

<150> KR 10-2004-0003610

<151> 2004-01-17

<150> KR 10-2004-0003957

<151> 2004-01-19

<160> 45

<170> PatentIn version 3.3

<210> 1

<211> 105

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> PEPTIDE

<222> (1)..(105)

<223> TFP1

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 20 25 30

Ala Asp Leu Ser Ser Ile Thr Ser Val Ser Ser Ala Ser Ala Ser Ala
 35 40 45

Thr Ala Ser Asp Ser Leu Ser Ser Ser Asp Gly Thr Val Tyr Leu Pro

50

55

60

Ser Thr Thr Ile Ser Gly Asp Leu Thr Val Thr Gly Lys Val Ile Ala
 65 70 75 80

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 85 90 95

Gly Glu Lys Tyr Val Phe Ser Ser Asp
 100 105

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 aatcgtttta acaaattcca agctgctgtc gctttggccc tactctctcg cggcgctctc 180
 ggtgactctt acaccaatag cacctctctc gcagacttga gttctatcac ttccgtctcg 240
 tcagctagtg caagtgccac cgcttccgac tcactttctt ccagtgacgg taccgtttat 300
 ttgccatcca caacaattag cggatgatctc acagttactg gtaaagtaat tgcaaccgag 360
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 <223> TFP2

<400> 3

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Val Ser Ala Leu Gln Val Asn Asn Ser Cys Val Ala Phe Pro Pro Ser
20 25 30

Asn Leu Arg Gly Lys Asn Gly Asp Gly Thr Asn Glu Gln Tyr Ala Thr
35 40 45

Ala Leu Leu Ser Ile Pro Trp Asn Gly Pro Pro Glu Ser Leu Arg Asp
50 55 60

Ile Asn Leu Ile Glu Leu Glu Pro Gln Val Ala Leu Tyr Leu Leu Glu
65 70 75 80

Asn Tyr Ile Asn His Tyr Tyr Asn Thr Thr Arg Asp Asn Lys Cys Pro
85 90 95

Asn Asn His Tyr Leu Met Gly Gly Gln Leu Gly Ser Ser Ser Asp Asn
100 105 110

Arg Ser Leu Asn Asp
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<213> *Saccharomyces cerevisiae*

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gtgagcgcac tccaggtcaa caattcatgt gtcgcttttc cgccatcaaa tctcagaggc 180
aaaaatggag acggtactaa tgaacagtat gcaactgcac tactttctat tccttgaat 240
ggacctcctg agtcattgag ggatattaat cttattgaac tcgaaccgca agttgcactc 300
tatttgctcg aaaattatat taaccattac tacaacacca caagagacaa taagtgcct 360
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<223> TFP3

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20 25 30

Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
35 40 45

Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
50 55 60

Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
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85 90 95

Thr Pro Thr Ser Ser Glu Lys Ile
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acgtccacaa acaaaaacaa aaataagaaa taggttgaca gtgggtgaaa aattctcgaa     180
ggtttcatct ccaaacagtc agtatataag tattcgggaa agagagccaa tctatcttgt     240
ggtggtgcta tcttaacctt ctcttttttg cagtagtaat tgtaaatcaa gacacataaa     300
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tccgttgctg ctctatccgc cactgcttct gctgaagggtt acactccagg tgaaccatgg    420
tccaccttaa cccaaccgg ctccatctct tgtgggtgctg ccgaatacac taccaccttt    480
ggatttgctg ttcaagctat tacctcttca aaagctaaga gagacgttat ctctcaaatt     540
ggtgacggtc aagtccaagc cacttctgct gctactgctc aagccaccga tagtcaagcc     600
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<213> Hansenula polymorpha

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Met Ala Ala Pro Val Glu Ser Leu Ala Gly Thr Gln Arg Tyr Leu Val
          20           25           30

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Gln Met Lys Glu Arg Phe Thr Thr Glu Lys Leu Cys Ala Leu Asp Asp
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Lys Ile
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<212> DNA
<213> Hansenula polymorpha

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<220>
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 ccacgttagg cgggggggatg gctgcaccgg ttgagtctct ggccgggacc caacggtatc 120

 tgggtgcaaat gaaggagcgg ttcaccacag agaagctgtg tgctttggac gacaagatc 179

<210> 9
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 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <221> PEPTIDE
 <222> (1)..(71)
 <223> TFP1-3

<400> 9

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 20 25 30

 Ala Asp Leu Ser Ser Ile Thr Ser Val Ser Ser Ala Ser Ala Ser Ala
 35 40 45

 Thr Ala Ser Asp Ser Leu Ser Ser Ser Asp Gly Thr Val Tyr Leu Pro
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 Ser Thr Thr Ile Ser Gly Asp
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acttcctgtc cgtcagctag tgcaagtgcc accgcttcgc actcacttcc ttccagtgc 180
ggtagcggtt atttgccatc cacaacaatt agcgggtgat tcacagttac tggtaaagta 240
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aaatacgtct tctcatctga tcctctaga 329

<210> 11
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<212> DNA
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<223> JH97(Sfi-HSA-forward primer)

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<210> 12
<211> 29
<212> DNA
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<210> 13
<211> 50
<212> DNA
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<223> JH99(Sfi-INV-forward primer)

<400> 13
gggcggccgc ctggcccta gataaaaggt caatgacaaa cgaaactagc 50

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<210> 15
<211> 37
<212> DNA
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<210> 16
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<212> DNA
<213> Artificial Sequence

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<223> JH107(Sfi-IL2-reverse primer)

<400> 16
gcggccatta cggccgtgca cctacttcaa gttctac 37

<210> 17
<211> 26
<212> DNA
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<223> JH120(BamHI-IL2-1-forward primer)

<400> 17
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<210> 18
<211> 27
<212> DNA
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<223> JH121(BamHI-IL2-2-forward primer)

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<210> 19
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<212> DNA

<213> Artificial Sequence

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<223> JH122(BamHI-IL2-3-forward primer)

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cgggatcctt gcacctactt caagttct 28

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<211> 22

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<223> JH123(INV-1-reverse primer)

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<210> 21

<211> 22

<212> DNA

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<223> JH124(INV-forward primer)

<400> 21

atattgttg ttccttcaat gg 22

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<211> 29

<212> DNA

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<223> JH95(INV-2-reverse primer)

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<212> DNA

<213> Artificial Sequence

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<223> JH132(SacI-GAL-forward primer)

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gggagctcat cgcttcgctg att 23

<210> 24
 <211> 27
 <212> DNA
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 <223> JH137(IL-2-Term-reverse primer)

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 ccgtcgactt aagttagtgt tgagatg 27

 <210> 25
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 <223> HY22(TFP1-LDKR-reverse primer)

 <400> 25
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 <211> 46
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 <210> 27
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 <212> DNA
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 <223> HY20(TFP2-LDKR-reverse primer)

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 <210> 28
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 <223> HY21(TFP2-LDKR-forward primer)

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<223> HY24(TFP4-LDKR-reverse primer)

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<212> DNA

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<223> HY25(TFP4-LDKR-forward primer)

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<223> JH143(XbaI-TFPl-d-reverse primer)

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<223> JH141(XbaI-TFP1-b-reverse primer)

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<210> 36
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<212> DNA
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<210> 38
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<212> DNA

<213> Artificial Sequence

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<223> HY17(TFP3-LDKR-reverse primer)

<400> 38

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<211> 43

<212> DNA

<213> Artificial Sequence

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<223> HY18(TFP3-LDKR-forward primer)

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20 25 30

Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
35 40 45

Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
50 55 60

Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
65 70 75 80

Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala
85 90 95

Thr Pro Thr Ser Ser Glu Lys Ile Ser Ser Ser Ala Ser Lys Thr Ser
100 105 110

Thr Asn Ala Thr Ser Ser Ser Cys Ala Thr Pro Ser Leu Lys Asp Ser
115 120 125

Ser Cys Lys Asn Ser Gly
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tgtgggtgctg ccgaatacac taccaccttt ggtattgctg ttcaagctat tacctcttca 180
aaagctaaga gagacgttat ctctcaaatt ggtgacggtc aagtccaagc cacttctgct 240
gctactgctc aagccaccga tagtcaagcc caagctacta ctaccgctac cccaaccagc 300
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20 25 30

Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
35 40 45

Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
50 55 60

Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
65 70 75 80

Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala
85 90 95

Thr Pro Thr Ser Ser Glu Lys Ile Ser Ser Ser Ala Ser Lys Thr Ser
100 105 110

Thr Asn Ala Thr Ser Ser Ser Cys Ala Thr Pro Ser Leu Lys Asp Ser
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Ser Cys Lys Asn Ser Gly Thr Leu Glu Leu Thr Leu Lys Asp Gly
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tgtggtgctg ccgaatacac ta